B1 Serial Nos. 08/003,257 and 08/003,389 are also continuation-in-parts of Serial No. 07/654,226. Each of these applications is incorporated by reference herein in their entireties --.

Please delete the paragraph spanning page 24, line 23 through page 25, line 19 and insert therefor:

--The protein encoded by *D. immitis* p4 is further characterized by having an LDL receptor-related protein (LDLr) class A cysteine-rich motif of about 9 amino acids that is also found in several other proteins, including mammalian low density lipoprotein (LDL) receptors, LDL receptor-related proteins, human and mouse alpha-2-macroglobulin receptors and rat renal GP 330 glycoprotein. Each of these proteins, including *D. immitis* P4, share the sequence DDCGDGSDE (i.e., Aspartic Acid -- Aspartic Acid -- Cysteine -- Glycine -- Aspartic Acid -- Glycine -- Serine -- Aspartic Acid -- Glutamic Acid), denoted herein as SEQ ID NO:5. A conserved stretch of eight of the nine amino acids is also found in the free-living (i.e., non-parasitic) nematode *Caenorhabditis elegans* LDL receptor-related protein and *C. elegans* basement membrane proteoglycan. This LDLr class A, cysteine-rich motif is likely to be conserved in proteins encoded by p4-related sequences of other helminths (i.e., nucleic acid sequences that hybridize under stringent conditions with *D. immitis* p4). As such, p4-related nucleic acid sequences may be identified using oligonucleotide probes that encode such LDLr class A motifs. Furthermore, the LDLr class A motif in P4-related proteins represents a target for development of therapeutic compositions to protect animals from parasitic helminth infection, as discussed below.--

B2

On page 68, please delete the paragraph spanning lines 2-24 and insert therefor:

--The chromatogram depicting the tryptic fragments of P22U is shown in FIG. 2. The fragments indicated by asterisks were submitted for sequencing. All sequencing was conducted at Macromolecular Resources, Department of Biochemistry, Colorado State University, Fort Collins, Colorado. The peptides were concentrated to 50 µl or less using a Speedvac® and frozen at about -20°C until sequencing. N-terminal sequencing was conducted in an ABI Model 473A Protein/ Peptide Sequencer System (Applied Biosystems, Inc., Foster City, California) using pulsed liquid chemistry and on line microgradient PTH amino acid analysis (see, for example, Hewick et. al., 1981, *J. Biol. Chem.* 256, p. 7990-7997; Geisow and Aitken, 1989, in Findlay, J.B.C. and M.J. Geisow (ed.). *Protein Sequencing: A Practical Approach*, p. 85-98). The most likely sequence of

B3

the tryptic fragment eluting at 44 minutes (referred to as the 44 min tryptic fragment), using one-letter amino acid code, was MAQDAFPNACAQGEPK (SEQ ID NO:6). The most likely sequence of the tryptic fragment eluting at 58 minutes (referred to as the 58 min tryptic fragment) was AIAPCQLTAVQSVLPCADQCQK (SEQ ID NO:7). The most likely sequence of the tryptic fragment eluting at 60 minutes (referred to as the 60 min tryptic fragment) was LGSCSPDCGLDLPSDNVMVQDV (SEQ ID NO:8).--

On page 71, please delete the paragraph spanning lines 10-22 and insert therefor:

--A homology search of the non-redundant protein sequence database was performed through the National Center for Biotechnology Information using the BLAST network. This database includes SwissProt + PIR + SPUpdate + GenPept + GPUpdate. The search was performed using SEQ ID NO:2 and showed the only significant homology shared between SEQ ID NO:2 and known sequences to be a contiguous stretch of 9 amino acids, namely DDCGDGSDE (SEQ ID NO:5), that was also found in human LDL-receptor related protein, human and mouse alpha-2-macroglobulin receptors and rat renal GP 330 glycoprotein. A conserved stretch of eight of the nine amino acids is also found in *Caenorhabditis elegans* LDL receptor-related protein and *C. elegans* basement membrane proteoglycan.--

Please delete the paragraph spanning page 71, line 26 through page 72, line 18 and insert therefor:

--Recombinant molecule pET19b-p4$_{635}$, containing *D. immitis* p4 nucleotides from about 1 through about 635 operatively linked to bacteriophage T7*lac* transcription control sequences and to a fusion sequence encoding a poly-histidine segment comprising 10 histidines was produced in the following manner. An about 635-nucleotide DNA fragment containing nucleotides spanning from about 1 through about 635 of SEQ ID NO:1, called p4$_{635}$, was PCR amplified from a clone containing *D. immitis* p4 using the primers 5' CGGGATCCCGAGTTAAATAGTCG 3' (denoted SEQ ID NO:9 or 394-5'; *Bam*HI site underlined) and 5' TGCAGGATCCTGCACCG 3' (denoted SEQ ID NO:10 or 394-3'; *Bam*HI site underlined). The PCR product was digested with *Bam*HI restriction endonuclease, gel purified and subcloned into expression vector pET19b (available from Novagen Inc., Madison, WI) that had been cleaved with *Bam*HI. The resulting recombinant molecule pET19b-p4$_{635}$ was transformed into *E. coli* BL21(DE3)pLysS to form recombinant cell *E.*

coli:pET19b-p4$_{635}$. *E. coli* BL21(DE3)pLysS includes a bacteriophage T7 RNA polymerase gene under the control of *lac* transcription control sequences.--

On page 74, please delete the paragraph spanning lines 2-27 and insert therefor:

--A segment of DNA for use in the identification of a nucleic acid sequence capable of encoding at least a portion of P22U was produced by PCR amplification using standard techniques, such as those described in Sambrook et al., *ibid.* Briefly, first strand cDNA was synthesized from adult female poly A+ RNA using Murine Leukemia Virus reverse transcriptase (available from Stratagene) and Stratagene's linker-primer from their ZAP-cDNA Synthesis Kit, namely 5' GAGAGAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTT- TTTTTTTT 3' (SEQ ID NO:11). A pool of two sets of degenerate primers was produced based on the partial amino acid sequence of the 60 min tryptic fragment described in Example 3. One degenerate set of primers, denoted GRF 11, includes the following sequences: 5'TGYTCNCCNGAYTGYGG 3' (SEQ ID NO:12), wherein Y can be either C or T, and N can be either A, G, C or T. The second set of primers, denoted GRF 12, includes the following sequences: 5'TGYAGTCCNGAYTGYGG 3' (SEQ ID NO:13). PCR amplification using the pool of degenerate primers in combination with Stratagene's linker-primer as the antisense primer was used to amplify the DNA segment. Verification that the appropriate segment had been amplified was accomplished by Southern blot analysis using a degenerate probe based on a more C-terminal amino acid sequence of the 60 min tryptic fragment, namely GRF 3 which includes the following sequences: 5' TGNACCATNACRTTRTC 3' (SEQ ID NO:14), wherein R can be either A or G.--

On page 75, please delete the paragraph spanning lines 9-20 and insert therefor:

--The adult female cDNA library was screened with an antisense probe, using stringent (i.e., standard) hybridization conditions as described in Sambrook et al., *ibid.*. The antisense probe, denoted GRF14, was based on the DNA sequence derived from the amplified segment and has the sequence 5' CTGTTTGAACCATAACATTATCAGATGG 3' (SEQ ID NO:15). Plaques which hybridized to the probe were rescreened, plaque purified and clones containing *D. immitis* nucleic acid sequence p22U (i.e., clones that hybridized with the antisense probe and having the apparent nucleic acid sequence designated in SEQ ID NO:3) were submitted to nucleic acid sequencing as described in Example 4.--